Listing of Claims:

1-37. (Canceled)

38. (Previously Added) A method for detecting the presence of at least one selected strain of human papilloma virus (HPV) in a sample, comprising:

providing a sample that may include nucleic acid from at least one selected strain of HPV and nucleic acid from at least one non-selected strain of HPV;

providing a plurality of primers substantially complementary to regions of both the nucleic acid from at least one selected strain of HPV and the nucleic acid from at least one non-selected strain of HPV;

exposing the sample to at least one probe that is sufficiently complementary to a portion of the nucleic acid from at least one non-selected strain to block full length amplification of the nucleic acid from at least one non-selected strain between the plurality of primers, the at least one probe comprising a nucleic acid analog comprising PNA;

amplifying said nucleic acid from at least one selected strain between said plurality of primers; and

detecting amplification product of nucleic acid from at least one selected strain.

39. (Previously Added) The method of claim 38, wherein the sample is derived from a subject and the selected strain indicates a risk of cancerous growth in the subject.

40. (Previously Amended) The method of claim 38, wherein the at least one probe is a hybrid further comprising a nucleic acid other than PNA.

41. (Previously Amended) The method of claim 38, wherein the step of amplifying said nucleic acid of at least one selected strain between said plurality of primers comprises conducting a reaction selected from the group consisting of a polymerase chain reaction, a ligase chain reaction, a rolling circle replication, a branched chain amplification, a nucleic acid based sequence amplification (NASBA), a Cleavase Fragment Length Polymorphism, ICAN, and RAM.

42. (Previously Added) The method of claim 38, wherein the regions of both the nucleic acids are parts of a region selected from the group consisting of L1, L2, E1, E6, and E7 region.

43. (Previously Added) The method of claim 38, wherein the at least one non-selected strain comprises all known low-risk HPV strains.

44. (Previously Added) The method of claim 38, wherein the at least one non-selected strain is selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.

45. (Previously Added) The method of claim 38, wherein the at least one selected strain comprises a plurality of high-risk HPV strains.

46. (Previously Amended) The method of claim 38, wherein the plurality of primers comprise MY09 (SEQ. ID. NO. 10) and MY11 (SEQ. ID. NO. 11).

47. (Previously Added) The method of claim 38, wherein the at least one probe is selected from the group of sequences consisting of SEQ. ID. NO. 6 and SEQ. ID. NO. 7.

48. (Previously Added) The method of claim 38, wherein the sample is a cervical scraping.

49. (Previously Added) The method of claim 38, wherein the step of detecting amplification product comprises in-gel electrophoresis of the product and staining the product with ethidium bromide.

50. (new) A method for detecting whether at least one selected strain of human papilloma virus (HPV) is present in a sample, comprising:

providing a sample that may include nucleic acid from at least one selected strain of HPV and may include nucleic acid from at least one non-selected strain of HPV;

providing at least one primer substantially complementary to a region in both the nucleic acid from at least one selected strain of HPV and the nucleic acid from at least one non-selected strain of HPV;

providing at least one probe that is sufficiently complementary to a portion of the nucleic acid from at least one non-selected strain to block amplification of the nucleic acid from at least one non-selected strain, the at least one probe comprising PNA;

exposing the sample to said at least one primer and said at least one probe under conditions in which at least a part of said region of said at least one selected strain of HPV, if present, will be amplified to produce an amplification product; and

detecting whether the amplification product is produced.

51. (new) The method of claim 50, wherein at least one of said at least one selected strain comprises a pathogenic strain.

52. (new) The method of claim 51, wherein said sample is derived from a subject and said pathogenic strain indicates a risk of cancerous growth in said subject.

53. (new) The method of claim 50, wherein at least one of said at least one probe is a hybrid further comprising a nucleic acid other than PNA.

54. (new) The method of claim 50, wherein at least one of said at least one probe comprises at least 8 bases.

55. (new) The method of claim 50, wherein the conditions in which at least a part of said region of said at least one selected strain of HPV, if present, will be amplified comprise conducting a reaction selected from the group consisting of a polymerase chain reaction, a ligase chain reaction, a rolling circle replication, a branched chain amplification, a nucleic acid based sequence amplification (NASBA), a Cleavase Fragment Length Polymorphism, ICAN, and RAM.

56. (new) The method of claim 55, wherein the conditions comprise conducting a polymerase chain reaction, and said at least one primer comprises a primer pair suitable for amplifying said at least a part of said region.

57. (new) The method of claim 55, wherein the conditions comprise conducting a ligase chain reaction.

58. (new) The method of claim 55, wherein the conditions comprise conducting a rolling circle replication.

59. (new) The method of claim 50, wherein at least one of said at least one primer is substantially complementary to a region of the HPV genome selected from L1, L2, E1, E6, and E7.

60. (new) The method of claim 59, wherein said region of the HPV genome is L1.

61. (new) The method of claim 59, wherein said region of the HPV genome is E6.

62. (new) The method of claim 50, wherein said at least one non-selected strain comprises a plurality of low-risk HPV strains.

63. (new) The method of claim 50, wherein said at least one non-selected strain comprises at least one strain selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.

64. (new) The method of claim 50, wherein said at least one selected strain comprises a plurality of high-risk HPV strains.

65. (new) The method of claim 50, wherein said at least one selected strain comprises at least one strain selected from the group consisting of HPV strains 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70.

66. (new) The method of claim 50, wherein said at least one primer comprises MY09 (SEQ. ID. NO. 10) and MY11 (SEQ. ID. NO. 11).

67. (new) The method of claim 50, wherein said at least one probe comprises at least one probe selected from SEQ. ID. NO. 6 and SEQ. ID. NO. 7.

68. (new) The method of claim 67, wherein said at least one probe comprises SEQ. ID. NO. 6.

69. (new) The method of claim 67, wherein said at least one probe comprises SEQ. ID. NO. 7.

70. (new) The method of claim 50, wherein said sample is a cervical scraping.

71. (new) The method of claim 50, wherein detecting whether said amplification product is produced comprises in-gel electrophoresis and staining with ethidium bromide.

72. (new) The method of claim 50, wherein a plurality of probes are provided, wherein each of said plurality is sufficiently complementary to a portion of the nucleic acid from a different non-selected strain.

73. (new) The method of claim 50, wherein at least one of said at least one probe is substantially complementary to a portion of nucleic acid that is adjacent to the region of nucleic acid to which at least one of said at least one primer is substantially complementary.

74. (new) A method for detecting whether at least one selected strain of human papilloma virus (HPV) is present in a sample, comprising:

providing a sample that may include nucleic acid from at least one selected strain of HPV and may include nucleic acid from at least one non-selected strain of HPV;

providing at least one primer substantially complementary to a region in both the nucleic acid from at least one selected strain of HPV and the nucleic acid from at least one non-selected strain of HPV;

providing at least one probe that is sufficiently complementary to a portion of the nucleic acid from at least one non-selected strain to block amplification of the nucleic acid from at least

one non-selected strain, the at least one probe comprising PNA selected from the group of sequences consisting of SEQ. ID. NO. 6 and SEQ. ID. NO. 7;

exposing the sample to said at least one primer and said at least one probe under conditions in which at least a part of said region of said at least one selected strain of HPV, if present, will be amplified to produce an amplification product; and

detecting whether the amplification product is produced.